(c) substituting the small DNA sequence between the unique ClaI and KpnI restriction sites with the oligonucleotide having the sequence of SEQ ID NO: 388.

SEQ ID NO: 386:

```
     AatII
5'  CTAATTCCGCTCTCACCTACCAAACAATGCCCCCCTGCAAAAAATAAATTCATAT-
3'  TGCAGATTAAGGCGAGAGTGGATGGTTTGTTACGGGGGGACGTTTTTTATTTAAGTATA-

    -AAAAAACATACAGATAACCATCTGCGGTGATAAATTATCTCTGGCGGTGTTGACATAAA-
    -TTTTTTGTATGTCTATTGGTAGACGCCACTATTTAATAGAGACCGCCACAACTGTATTT-

    -TACCACTGGCGGTGATACTGAGCACAT     3'
    -ATGGTGACCGCCACTATGACTCGTGTAGC   5'
                 ClaI
```

SEQ ID NO: 387:

```
5'  CGATTTGATTCTAGAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGGTAC  3'
3'    TAAACTAAGATCTTCCTCCTTATTGTATACCAATTGCGCAACCTTAAGC       5'
    ClaI                                                KpnI
```

The expression plasmid pAMG21 can then be derived from pCFM1656 by making a series of site-directed base changes by PCR overlapping oligo mutagenesis and DNA sequence substitutions. Starting with the BglII site (plasmid bp # 180) immediately 5' to the plasmid replication promoter P_{copB} and proceeding toward the plasmid replication genes, the base pair changes are as shown in Table B below.

Table B—Base pair changes resulting in pAMG21

pAMG21 bp #	bp in pCFM1656	bp changed to in pAMG21
# 204	T/A	C/G
# 428	A/T	G/C
# 509	G/C	A/T
# 617	- -	insert two G/C bp
# 679	G/C	T/A
# 980	T/A	C/G
# 994	G/C	A/T
# 1004	A/T	C/G
# 1007	C/G	T/A
# 1028	A/T	T/A
# 1047	C/G	T/A
# 1178	G/C	T/A
# 1466	G/C	T/A
# 2028	G/C	bp deletion
# 2187	C/G	T/A
# 2480	A/T	T/A
# 2499-2502	AGTG TCAC	GTCA CAGT
# 2642	TCCGAGC AGGCTCG	7 bp deletion
# 3435	G/C	A/T
# 3446	G/C	A/T
# 3643	A/T	T/A

The DNA sequence between the unique AatII (position #4364 in pCFM1656) and SacII (position #4585 in pCFM1656) restriction sites is substituted with the DNA sequence (SEQ ID NO: 23) shown in Figures 17A and 17B. During the ligation of the sticky ends of this substitution DNA sequence, the outside AatII and SacII sites are destroyed. There are unique AatII and SacII sites in the substituted DNA.

GM221 (Amgen #2596). The Amgen host strain #2596 is an E.coli K-12 strain derived from Amgen strain #393. It has been modified to contain both the temperature sensitive lambda repressor cI857s7 in the early ebg region and the $lacI^Q$ repressor in the late ebg region (68 minutes). The presence of these two repressor genes allows the use of this host with a variety of expression systems, however both of these repressors are irrelevant to the expression from $luxP_R$. The untransformed host has no antibiotic resistances.

The ribosome binding site of the cI857s7 gene has been modified to include an enhanced RBS. It has been inserted into the ebg operon between nucleotide position 1170 and 1411 as numbered in Genbank accession number M64441Gb_Ba with deletion of the intervening ebg sequence. The sequence of the insert is shown below with lower case letters representing the ebg sequences flanking the insert shown below (SEQ ID NO: 388):

```
ttattttcgtGCGGCCGCACCATTATCACCGCCAGAGGTAAACTAGTCAACACGCACGGTGTTAGATATTTAT
CCCTTGCGGTGATAGATTGAGCACATCGATTTGATTCTAGAAGGAGGGATAATATATGAGCACAAAAAAGAAA
CCATTAACACAAGAGCAGCTTGAGGACGCACGTCGCCTTAAAGCAATTTATGAAAAAAAGAAAAATGAACTTG
GCTTATCCCAGGAATCTGTCGCAGACAAGATGGGGATGGGGCAGTCAGGCGTTGGTGCTTTATTTAATGGCAT
CAATGCATTAAATGCTTATAACGCCGCATTGCTTACAAAAATTCTCAAAGTTAGCGTTGAAGAATTTAGCCCT
TCAATCGCCAGAGAATCTACGAGATGTATGAAGCGGTTAGTATGCAGCCGTCACTTAGAAGTGAGTATGAGTA
CCCTGTTTTTTCTCATGTTCAGGCAGGGATGTTCTCACCTAAGCTTAGAACCTTTACCAAAGGTGATGCGGAG
AGATGGGTAAGCACAACCAAAAAAGCCAGTGATTCTGCATTCTGGCTTGAGGTTGAAGGTAATTCCATGACCG
CACCAACAGGCTCCAAGCCAAGCTTTCCTGACGGAATGTTAATTCTCGTTGACCCTGAGCAGGCTGTTGAGCC
AGGTGATTTCTGCATAGCCAGACTTGGGGGTGATGAGTTTACCTTCAAGAAACTGATCAGGGATAGCGGTCAG
GTGTTTTTACAACCACTAAACCCACAGTACCCAATGATCCCATGCAATGAGAGTTGTTCCGTTGTGGGGAAAG
TTATCGCTAGTCAGTGGCCTGAAGAGACGTTTGGCTGATAGACTAGTGGATCCACTAGTgtttctgccc
```

The construct was delivered to the chromosome using a recombinant phage called MMebg-cI857s7enhanced RBS #4 into F'tet/393. After recombination and resolution only the chromosomal insert described

above remains in the cell. It was renamed F'tet/GM101. F'tet/GM101 was then modified by the delivery of a $lacI^Q$ construct into the ebg operon between nucleotide position 2493 and 2937 as numbered in the Genbank accession number M64441Gb_Ba with the deletion of the intervening ebg sequence. The sequence of the insert is shown below with the lower case letters representing the ebg sequences flanking the insert (SEQ ID NO: 389) shown below:

```
ggcggaaaccGACGTCCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGAGTCA
ATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCGGTGTCTCTTATCAGACC
GTTTCCCGCGTGGTGAACCAGGCCAGCCACGTTTCTGCGAAAACGCGGGAAAAAGTCGAAGCGGCGATGGCGG
AGCTGAATTACATTCCCAACCGCGTGGCACAACAACTGGCGGGCAAACAGTCGCTCCTGATTGGCGTTGCCAC
CTCCAGTCTGGCCCTGCACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCC
AGCGTGGTGGTGTCGATGGTAGAACGAAGCGGCGTCGAAGCCTGTAAAGCGGCGGTGCACAATCTTCTCGCGC
AACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCATTGCTGTGGAAGCTGCCTGCAC
TAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTATTTTCTCCCATGAAGAC
GGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAA
GTTCTGTCTCGGCGCGTCTGCGTCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAGC
GGAACGGGAAGGCGACTGGAGTGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGAATGAGGGCATCGTT
CCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAATGCGCGCCATTACCGAGTCCGGGCTGC
GCGTTGGTGCGGATATCTCGGTAGTGGGATACGACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAAC
CACCATCAAACAGGATTTTCGCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAG
GCGGTGAAGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACCCTGGCGCCCAATACGCAAA
CCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGACA
GTAAGGTACCATAGGATCCaggcacagga
```

The construct was delivered to the chromosome using a recombinant phage called AGebg-LacIQ#5 into F'tet/GM101. After recombination and resolution only the chromosomal insert described above remains in the cell. It was renamed F'tet/GM221. The F'tet episome was cured from the strain using acridine orange at a concentration of 25 μg/ml in LB. The cured strain was identified as tetracyline sensitive and was stored as GM221.

Expression. Cultures of pAMG21-Fc-TMP-TMP in *E. coli* GM221 in Luria Broth medium containing 50 μg/ml kanamycin were incubated at 37°C prior to induction. Induction of Fc-TMP-TMP gene product expression from the luxPR promoter was achieved following the addition of the synthetic autoinducer N-(3-oxohexanoyl)-DL-homoserine lactone to the culture media to a final concentration of 20 ng/ml and cultures were incubated at 37°C for a further 3 hours. After 3 hours, the bacterial

cultures were examined by microscopy for the presence of inclusion bodies and were then collected by centrifugation. Refractile inclusion bodies were observed in induced cultures indicating that the Fc-TMP-TMP was most likely produced in the insoluble fraction in *E. coli*. Cell pellets were lysed directly by resuspension in Laemmli sample buffer containing 10% •-mercaptoethanol and were analyzed by SDS-PAGE. An intense Coomassie stained band of approximately 30kDa was observed on an SDS-PAGE gel. The expected gene product would be 269 amino acids in length and have an expected molecular weight of about 29.5 kDa. Fermentation was also carried out under standard batch conditions at the 10 L scale, resulting in similar expression levels of the Fc-TMP-TMP to those obtained at bench scale.

Purification of Fc-TMP-TMP. Cells are broken in water (1/10) by high pressure homogenization (2 passes at 14,000 PSI) and inclusion bodies are harvested by centrifugation (4200 RPM in J-6B for 1 hour). Inclusion bodies are solubilized in 6M guanidine, 50mM Tris, 8mM DTT, pH 8.7 for 1 hour at a 1/10 ratio. The solubilized mixture is diluted 20 times into 2M urea, 50 mM tris, 160mM arginine, 3mM cysteine, pH 8.5. The mixture is stirred overnight in the cold and then concentrated about 10 fold by ultafiltration. It is then diluted 3 fold with 10mM Tris, 1.5M urea, pH 9. The pH of this mixture is then adjusted to pH 5 with acetic acid. The precipitate is removed by centrifugation and the supernatant is loaded onto a SP-Sepharose Fast Flow column equilibrated in 20mM NaAc, 100 mM NaCl, pH 5(10mg/ml protein load, room temperature). The protein is eluted off using a 20 column volume gradient in the same buffer ranging from 100mM NaCl to 500mM NaCl. The pool from the column is diluted 3 fold and loaded onto a SP-Sepharose HP column in 20 mM NaAc, 150 mM NaCl, pH 5(10 mg/ml protein load, room temperature). The protein is eluted off using a 20 column volume gradient

in the same buffer ranging from 150 mM NaCl to 400 mM NaCl. The peak is pooled and filtered.

Characterization of Fc-TMP activity. The following is a summary of in vivo data in mice with various compounds of this invention.

Mice: Normal female BDF1 approximately 10-12 weeks of age.

Bleed schedule: Ten mice per group treated on day 0, two groups started 4 days apart for a total of 20 mice per group. Five mice bled at each time point, mice were bled a minimum of three times a week. Mice were anesthetized with isoflurane and a total volume of 140-160 µl of blood was obtained by puncture of the orbital sinus. Blood was counted on a Technicon H1E blood analyzer running software for murine blood. Parameters measured were white blood cells, red blood cells, hematocrit, hemoglobin, platelets, neutrophils.

Treatments: Mice were either injected subcutaneously for a bolus treatment or implanted with 7-day micro-osmotic pumps for continuous delivery. Subcutaneous injections were delivered in a volume of 0.2 ml. Osmotic pumps were inserted into a subcutaneous incision made in the skin between the scapulae of anesthetized mice. Compounds were diluted in PBS with 0.1% BSA. All experiments included one control group, labeled "carrier" that were treated with this diluent only. The concentration of the test articles in the pumps was adjusted so that the calibrated flow rate from the pumps gave the treatment levels indicated in the graphs.

Compounds: A dose titration of the compound was delivered to mice in 7 day micro-osmotic pumps. Mice were treated with various compounds at a single dose of 100 µg/kg in 7 day osmotic pumps. Some of the same compounds were then given to mice as a single bolus injection.

Activity test results: The results of the activity experiments are shown in Figures 11 and 12. In dose response assays using 7-day micro-

osmotic pumps, the maximum effect was seen with the compound of SEQ ID NO: 18 was at 100 μg/kg/day; the 10 μg/kg/day dose was about 50% maximally active and 1 μg/kg/day was the lowest dose at which activity could be seen in this assay system. The compound at 10 μg/kg/day dose was about equally active as 100 μg/kg/day unpegylated rHu-MGDF in the same experiment.

Example 3

Fc-EMP fusions

Fc-EMP. A DNA sequence coding for the Fc region of human IgG1 fused in-frame to a monomer of the EPO-mimetic peptide was constructed using standard PCR technology. Templates for PCR reactions were a vector containing the Fc sequence (pFc-A3, described in International application WO 97/23614, published July 3, 1997) and a synthetic gene encoding EPO monomer. The synthetic gene for the monomer was constructed from the 4 overlapping oligonucleotides (SEQ ID NOS: 390 to 393, respectively) shown below:

```
1798-2 TAT GAA AGG TGG AGG TGG TGG TGG AGG TAC TTA CTC TTG
       CCA CTT CGG CCC GCT GAC TTG G

1798-3 CGG TTT GCA AAC CCA AGT CAG CGG GCC GAA GTG GCA AGA
       GTA AGT ACC TCC ACC ACC ACC TCC ACC TTT CAT

1798-4 GTT TGC AAA CCG CAG GGT GGC GGC GGC GGC GGC GGT GGT
       ACC TAT TCC TGT CAT TTT

1798-5 CCA GGT CAG CGG GCC AAA ATG ACA GGA ATA GGT ACC ACC
       GCC GCC GCC GCC GCC ACC CTG
```

The 4 oligonucleotides were annealed to form the duplex encoding an amino acid sequence (SEQ ID NOS: 394 and 395, respectively) shown below:

```
   TATGAAAGGTGGAGGTGGTGGTGGAGGTACTTACTCTTGCCACTTCGGCCCGCTGACTTG
 1 ---------+---------+---------+---------+---------+---------+ 60
   TACTTTCCACCTCCACCACCACCTCCATGAATGAGAACGGTGAAGCCGGGCGACTGAAC
b   M  K  G  G  G  G  G  G  G  T  Y  S  C  H  F  G  P  L  T  W  -

   GGTTTGCAAACCGCAGGGTGGCGGCGGCGGCGGCGGTGGTACCTATTCCTGTCATTTT
61 ---------+---------+---------+---------+---------+---------+---------+-- 133
   CCAAACGTTTGGCGTCCCACCGCCGCCGCCGCCGCCACCATGGATAAGGACAGTAAAACCGGGCGACTGGACC
b   V  C  K  P  Q  G  G  G  G  G  G  G  G  T  Y  S  C  H  F   -
```

This duplex was amplified in a PCR reaction using

```
1798-18    GCA GAA GAG CCT CTC CCT GTC TCC GGG TAA
           AGG TGG AGG TGG TGG TGG AGG TAC TTA
           CTC T
```

and

```
1798-19    CTA ATT GGA TCC ACG AGA TTA ACC ACC
           CTG CGG TTT GCA A
```

as the sense and antisense primers (SEQ ID NOS: 396 and 397, respectively).

The Fc portion of the molecule was generated in a PCR reaction with pFc-A3 using the primers

1216-52	AAC ATA AGT ACC TGT AGG ATC G
1798-17	AGA GTA AGT ACC TCC ACC ACC ACC TCC ACC TTT ACC CGG AGA CAG GGA GAG GCT CTT CTG C

which are SEQ ID NOS: 398 and 399, respectively. The oligonucleotides 1798-17 and 1798-18 contain an overlap of 61 nucleotides, allowing the two genes to be fused together in the correct reading frame by combining the above PCR products in a third reaction using the outside primers, 1216-52 and 1798-19.

The final PCR gene product (the full length fusion gene) was digested with restriction endonucleases XbaI and BamHI, and then ligated into the vector pAMG21 (described below), also digested with XbaI and BamHI. Ligated DNA was transformed into competent host cells of E. coli strain 2596 (GM221, described herein). Clones were screened for the ability to produce the recombinant protein product and to possess the gene fusion having the correct nucleotide sequence. A single such clone was selected and designated Amgen strain #3718.

The nucleotide and amino acid sequence of the resulting fusion protein (SEQ ID NOS: 15 and 16) are shown in Figure 13.

EMP-Fc. A DNA sequence coding for a monomer of the EPO-mimetic peptide fused in-frame to the Fc region of human IgG1 was constructed using standard PCR technology. Templates for PCR reactions were the pFC-A3a vector and a synthetic gene encoding EPO monomer. The synthetic gene for the monomer was constructed from the 4 overlapping oligonucleotides 1798-4 and 1798-5 (above) and 1798-6 and 1798-7 (SEQ ID NOS: 400 and 401, respectively) shown below:

```
1798-6 GGC CCG CTG ACC TGG GTA TGT AAG CCA CAA GGG GGT GGG
       GGA GGC GGG GGG TAA TCT CGA G

1798-7 GAT CCT CGA GAT TAC CCC CCG CCT CCC CCA CCC CCT TGT
       GGC TTA CAT AC
```

The 4 oligonucleotides were annealed to form the duplex encoding an amino acid sequence (SEQ ID NOS: 402 and 403, respectively) shown below:

```
                GTTTGCAAACCGCAGGGTGGCGGCGGCGGCGGCGGTGGTACCTATTCCTGTCATTTTGGC
              1 ---------+---------+---------+---------+---------+---------+- 60
                         GTCCCACCGCCGCCGCCGCCGCCACCATGGATAAGGACAGTAAAACCG
A               V  C  K  P  Q  G  G  G  G  G  G  G  G  T  Y  S  C  H  F  G  -
                CCGCTGACCTGGGTATGTAAGCCACAAGGGGGTGGGGGAGGCGGGGGGTAATCTCGAG
             61 ---------+---------+---------+---------+---------+---------+- 122
                GGCGACTGGACCCATACATTCGGTGTTCCCCCACCCCCTCCGCCCCCCATTAGAGCTCCTAG
A               P  L  T  W  V  C  K  P  Q  G  G  G  G  G  G  G  *
```

This duplex was amplified in a PCR reaction using

```
1798-21       TTA TTT CAT ATG AAA GGT GGT AAC TAT TCC TGT CAT TTT
```

and

```
1798-22       TGG ACA TGT GTG AGT TTT GTC CCC CCC GCC TCC CCC ACC
              CCC T
```

as the sense and antisense primers (SEQ ID NOS: 404 and 405, respectively).

The Fc portion of the molecule was generated in a PCR reaction with pFc-A3 using the primers

```
1798-23       AGG GGG TGG GGG AGG CGG GGG GGA CAA AAC TCA CAC ATG
              TCC A
```

and

```
1200-54       GTT ATT GCT CAG CGG TGG CA
```

which are SEQ ID NOS: 406 and 407, respectively. The oligonucleotides 1798-22 and 1798-23 contain an overlap of 43 nucleotides, allowing the two genes to be fused together in the correct reading frame by combining the above PCR products in a third reaction using the outside primers, 1787-21 and 1200-54.

The final PCR gene product (the full length fusion gene) was digested with restriction endonucleases XbaI and BamHI, and then ligated

into the vector pAMG21 and transformed into competent E. coli strain 2596 cells as described above. Clones were screened for the ability to produce the recombinant protein product and to possess the gene fusion having the correct nucleotide sequence. A single such clone was selected and designated Amgen strain #3688.

The nucleotide and amino acid sequences (SEQ ID NOS: 17 and 18) of the resulting fusion protein are shown in Figure 14.

EMP-EMP-Fc. A DNA sequence coding for a dimer of the EPO-mimetic peptide fused in-frame to the Fc region of human IgG1 was constructed using standard PCR technology. Templates for PCR reactions were the EMP-Fc plasmid from strain #3688 above and a synthetic gene encoding the EPO dimer. The synthetic gene for the dimer was constructed from the 8 overlapping oligonucleotides (SEQ ID NOS:408 to 415, respectively) shown below:

1869-23	TTT TTT ATC GAT TTG ATT CTA GAT TTG AGT TTT AAC TTT TAG AAG GAG GAA TAA AAT ATG
1869-48	TAA AAG TTA AAA CTC AAA TCT AGA ATC AAA TCG ATA AAA AA
1871-72	GGA GGT ACT TAC TCT TGC CAC TTC GGC CCG CTG ACT TGG GTT TGC AAA CCG
1871-73	AGT CAG CGG GCC GAA GTG GCA AGA GTA AGT ACC TCC CAT ATT TTA TTC CTC CTT C
1871-74	CAG GGT GGC GGC GGC GGC GGC GGT GGT ACC TAT TCC TGT CAT TTT GGC CCG CTG ACC TGG
1871-75	AAA ATG ACA GGA ATA GGT ACC ACC GCC GCC GCC GCC GCC ACC CTG CGG TTT GCA AAC CCA
1871-78	GTA TGT AAG CCA CAA GGG GGT GGG GGA GGC GGG GGG GAC AAA ACT CAC ACA TGT CCA
1871-79	AGT TTT GTC CCC CCC GCC TCC CCC ACC CCC TTG TGG CTT ACA TAC CCA GGT CAG CGG GCC

The 8 oligonucleotides were annealed to form the duplex encoding an amino acid sequence (SEQ ID NOS: 416 and 417, respectively) shown below:

```
                TTTTTTATCGATTTGATTCTAGATTTGAGTTTTAACTTTTAGAAGGAGGAATAAAATATG
          1     ---------+---------+---------+---------+---------+---------+ 60
                AAAAAATAGCTAAACTAAGATCTAAACTCAAAATTGAAAATCTTCCTCCTTATTTTATAC
a                                                                   M    -
                                                                    |||
```

```
                GGAGGTACTTACTCTTGCCACTTCGGCCCGCTGACTTGGGTTTGCAAACCGCAGGGTGGC
           61   ---------+---------+---------+---------+---------+---------+ 120
                CCTCCATGAATGAGAACGGTGAAGCCGGGCGACTGAACCCAAACGTTTGGCGTCCCACCG
 5   a            G  G  T  Y  S  C  H  F  G  P  L  T  W  V  C  K  P  Q  G  G   -

                GGCGGCGGCGGCGGTGGTACCTATTCCTGTCATTTTGGCCCGCTGACCTGGGTATGTAAG
          121   ---------+---------+---------+---------+---------+---------+ 180
                CCGCCGCCGCCGCCACCATGGATAAGGACAGTAAAACCGGGCGACTGGACCCATACATTC
10   a            G  G  G  G  G  G  T  Y  S  C  H  F  G  P  L  T  W  V  C  K   -

                CCACAAGGGGGTGGGGGAGGCGGGGGGGACAAAACTCACACATGTCCA
          181   ---------+---------+---------+---------+--------- 228
                GGTGTTCCCCCACCCCCTCCGCCCCCCCTGTTTTGA
15   a            P  Q  G  G  G  G  G  G  G  D  K  T  H  T  C  P   -
```

This duplex was amplified in a PCR reaction using 1869-23 and 1871-79 (shown above) as the sense and antisense primers.

The Fc portion of the molecule was generated in a PCR reaction with strain 3688 DNA using the primers 1798-23 and 1200-54 (shown above).

The oligonucleotides 1871-79 and 1798-23 contain an overlap of 31 nucleotides, allowing the two genes to be fused together in the correct reading frame by combining the above PCR products in a third reaction using the outside primers, 1869-23 and 1200-54.

The final PCR gene product (the full length fusion gene) was digested with restriction endonucleases XbaI and BamHI, and then ligated into the vector pAMG21 and transformed into competent E. coli strain 2596 cells as described for Fc-EMP. Clones were screened for ability to produce the recombinant protein product and possession of the gene fusion having the correct nucleotide sequence. A single such clone was selected and designated Amgen strain #3813.

The nucleotide and amino acid sequences (SEQ ID NOS: 19 and 20, respectively) of the resulting fusion protein are shown in Figure 15. There is a silent mutation at position 145 (A to G, shown in boldface) such that the final construct has a different nucleotide sequence than the oligonucleotide 1871-72 from which it was derived.

Fc-EMP-EMP. A DNA sequence coding for the Fc region of human IgG1 fused in-frame to a dimer of the EPO-mimetic peptide was

constructed using standard PCR technology. Templates for PCR reactions were the plasmids from strains 3688 and 3813 above.

The Fc portion of the molecule was generated in a PCR reaction with strain 3688 DNA using the primers 1216-52 and 1798-17 (shown above). The EMP dimer portion of the molecule was the product of a second PCR reaction with strain 3813 DNA using the primers 1798-18 (also shown above) and SEQ ID NO: 418, shown below:

1798-20 CTA ATT GGA TCC TCG AGA TTA ACC CCC TTG TGG CTT ACAT

The oligonucleotides 1798-17 and 1798-18 contain an overlap of 61 nucleotides, allowing the two genes to be fused together in the correct reading frame by combining the above PCR products in a third reaction using the outside primers, 1216-52 and 1798-20.

The final PCR gene product (the full length fusion gene) was digested with restriction endonucleases XbaI and BamHI, and then ligated into the vector pAMG21 and transformed into competent E. coli strain 2596 cells as described for Fc-EMP. Clones were screened for the ability to produce the recombinant protein product and to possess the gene fusion having the correct nucleotide sequence. A single such clone was selected and designated Amgen strain #3822.

The nucleotide and amino acid sequences (SEQ ID NOS: __ and __, respectively) of the fusion protein are shown in Figure 16.

Characterization of Fc-EMP activity. Characterization was carried out in vivo as follows.

Mice: Normal female BDF1 approximately 10-12 weeks of age.

Bleed schedule: Ten mice per group treated on day 0, two groups started 4 days apart for a total of 20 mice per group. Five mice bled at each time point, mice were bled a maximum of three times a week. Mice were anesthetized with isoflurane and a total volume of 140-160 ml of blood was obtained by puncture of the orbital sinus. Blood was counted

on a Technicon H1E blood analyzer running software for murine blood. Parameters measured were WBC, RBC, HCT, HGB, PLT, NEUT, LYMPH.

Treatments: Mice were either injected subcutaneously for a bolus treatment or implanted with 7 day micro-osmotic pumps for continuous delivery. Subcutaneous injections were delivered in a volume of 0.2 ml. Osmotic pumps were inserted into a subcutaneous incision made in the skin between the scapulae of anesthetized mice. Compounds were diluted in PBS with 0.1% BSA. All experiments included one control group, labeled "carrier" that were treated with this diluent only. The concentration of the test articles in the pumps was adjusted so that the calibrated flow rate from the pumps gave the treatment levels indicated in the graphs.

Experiments: Various Fc-conjugated EPO mimetic peptides (EMPs) were delivered to mice as a single bolus injection at a dose of 100 μg/kg. Fc-EMPs were delivered to mice in 7-day micro-osmotic pumps. The pumps were not replaced at the end of 7 days. Mice were bled until day 51 when HGB and HCT returned to baseline levels.

Example 4

TNF-α inhibitors

Fc-TNF-α inhibitors. A DNA sequence coding for the Fc region of human IgG1 fused in-frame to a monomer of the TNF-α inhibitory peptide was constructed using standard PCR technology. The Fc and 5 glycine linker portion of the molecule was generated in a PCR reaction with DNA from the Fc-EMP fusion strain #3718 (see Example 3) using the sense primer 1216-52 and the antisense primer 2295-89 (SEQ ID NOS: 1112 and 1113 , respectively). The nucleotides encoding the TNF-α inhibitory peptide were provided by the PCR primer 2295-89 shown below:

```
1216-52      AAC ATA AGT ACC TGT AGG ATC G
2295-89      CCG CGG ATC CAT TAC GGA CGG TGA CCC AGA GAG GTG TTT TTG TAG
```

TGC GGC AGG AAG TCA CCA CCA CCT CCA CCT TTA CCC

The oligonucleotide 2295-89 overlaps the glycine linker and Fc portion of the template by 22 nucleotides, with the PCR resulting in the two genes being fused together in the correct reading frame.

The PCR gene product (the full length fusion gene) was digested with restriction endonucleases NdeI and BamHI, and then ligated into the vector pAMG21 and transformed into competent E. coli strain 2596 cells as described for EMP-Fc herein. Clones were screened for the ability to produce the recombinant protein product and to possess the gene fusion having the correct nucleotide sequence. A single such clone was selected and designated Amgen strain #4544.

The nucleotide and amino acid sequences (SEQ ID NOS: 1055 and 1056) of the fusion protein are shown in Figures 19A and 19B.

TNF-α inhibitor-Fc. A DNA sequence coding for a TNF-α inhibitory peptide fused in-frame to the Fc region of human IgG1 was constructed using standard PCR technology. The template for the PCR reaction was a plasmid containing an unrelated peptide fused via a five glycine linker to Fc. The nucleotides encoding the TNF-α inhibitory peptide were provided by the sense PCR primer 2295-88, with primer 1200-54 serving as the antisense primer (SEQ ID NOS: 1117 and 407, respectively). The primer sequences are shown below:

2295-88 GAA TAA CAT ATG GAC TTC CTG CCG CAC TAC AAA AAC ACC TCT CTG GGT CAC CGT CCG GGT GGA GGC GGT GGG GAC AAA ACT

1200-54 GTT ATT GCT CAG CGG TGG CA

The oligonucleotide 2295-88 overlaps the glycine linker and Fc portion of the template by 24 nucleotides, with the PCR resulting in the two genes being fused together in the correct reading frame.

The PCR gene product (the full length fusion gene) was digested with restriction endonucleases NdeI and BamHI, and then ligated into the vector pAMG21 and transformed into competent E. coli strain 2596 cells as described for EMP-Fc herein. Clones were screened for the ability to produce the recombinant protein product and to possess the gene fusion having the correct nucleotide sequence. A single such clone was selected and designated Amgen strain #4543.

The nucleotide and amino acid sequences (SEQ ID NOS: 1057 and 1058) of the fusion protein are shown in Figures 20A and 20B.

Expression in E. coli. Cultures of each of the pAMG21-Fc-fusion constructs in E. coli GM221 were grown at 37 °C in Luria Broth medium containing 50 mg/ml kanamycin. Induction of gene product expression from the luxPR promoter was achieved following the addition of the synthetic autoinducer N-(3-oxohexanoyl)-DL-homoserine lactone to the culture media to a final concentration of 20 ng/ml. Cultures were incubated at 37 °C for a further 3 hours. After 3 hours, the bacterial cultures were examined by microscopy for the presence of inclusion bodies and were then collected by centrifugation. Refractile inclusion bodies were observed in induced cultures indicating that the Fc-fusions were most likely produced in the insoluble fraction in E. coli. Cell pellets were lysed directly by resuspension in Laemmli sample buffer containing 10% β-mercaptoethanol and were analyzed by SDS-PAGE. In each case, an intense coomassie-stained band of the appropriate molecular weight was observed on an SDS-PAGE gel.

Purification of Fc-peptide fusion proteins. Cells are broken in water (1/10) by high pressure homogenization (2 passes at 14,000 PSI) and inclusion bodies are harvested by centrifugation (4200 RPM in J-6B for 1 hour). Inclusion bodies are solubilized in 6M guanidine, 50mM Tris, 8mM DTT, pH 8.7 for 1 hour at a 1/10 ratio. The solubilized mixture is diluted

20 times into 2M urea, 50 mM tris, 160mM arginine, 3mM cysteine, pH 8.5. The mixture is stirred overnight in the cold and then concentrated about 10 fold by ultafiltration. It is then diluted 3 fold with 10mM Tris, 1.5M urea, pH 9. The pH of this mixture is then adjusted to pH 5 with acetic acid. The precipitate is removed by centrifugation and the supernatant is loaded onto a SP-Sepharose Fast Flow column equilibrated in 20mM NaAc, 100 mM NaCl, pH 5 (10mg/ml protein load, room temperature). The protein is eluted from the column using a 20 column volume gradient in the same buffer ranging from 100mM NaCl to 500mM NaCl. The pool from the column is diluted 3 fold and loaded onto a SP-Sepharose HP column in 20mM NaAc, 150mM NaCl, pH 5(10mg/ml protein load, room temperature). The protein is eluted using a 20 column volume gradient in the same buffer ranging from 150mM NaCl to 400mM NaCl. The peak is pooled and filtered.

Characterization of activity of Fc-TNF-α inhibitor and TNF-α inhibitor -Fc. Binding of these peptide fusion proteins to TNF- α can be characterized by BIAcore by methods available to one of ordinary skill in the art who is armed with the teachings of the present specification.

Example 5

IL-1 Antagonists

Fc-IL-1 antagonist. A DNA sequence coding for the Fc region of human IgG1 fused in-frame to a monomer of an IL-1 antagonist peptide was constructed using standard PCR technology. The Fc and 5 glycine linker portion of the molecule was generated in a PCR reaction with DNA from the Fc-EMP fusion strain #3718 (see Example 3) using the sense primer 1216-52 and the antisense primer 2269-70 (SEQ ID NOS: 1112 and 1118, respectively). The nucleotides encoding the IL-1 antagonist peptide were provided by the PCR primer 2269-70 shown below:

1216-52 AAC ATA AGT ACC TGT AGG ATC G

2269-70 CCG CGG ATC CAT TAC AGC GGC AGA GCG TAC GGC TGC CAG TAA CCC
GGG GTC CAT TCG AAA CCA CCA CCT CCA CCT TTA CCC

The oligonucleotide 2269-70 overlaps the glycine linker and Fc portion of the template by 22 nucleotides, with the PCR resulting in the two genes being fused together in the correct reading frame.

The PCR gene product (the full length fusion gene) was digested with restriction endonucleases NdeI and BamHI, and then ligated into the vector pAMG21 and transformed into competent E. coli strain 2596 cells as described for EMP-Fc herein. Clones were screened for the ability to produce the recombinant protein product and to possess the gene fusion having the correct nucleotide sequence. A single such clone was selected and designated Amgen strain #4506.

The nucleotide and amino acid sequences (SEQ ID NOS: 1059 and 1060) of the fusion protein are shown in Figures 21A and 21B.

IL-1 antagonist-Fc. A DNA sequence coding for an IL-1 antagonist peptide fused in-frame to the Fc region of human IgG1 was constructed using standard PCR technology. The template for the PCR reaction was a plasmid containing an unrelated peptide fused via a five glycine linker to Fc. The nucleotides encoding the IL-1 antagonist peptide were provided by the sense PCR primer 2269-69, with primer 1200-54 serving as the antisense primer (SEQ ID NOS: 1119 and 407, respectively). The primer sequences are shown below:

2269-69 GAA TAA CAT ATG TTC GAA TGG ACC CCG GGT TAC TGG CAG CCG TAC GCT
CTG CCG CTG GGT GGA GGC GGT GGG GAC AAA ACT

1200-54 GTT ATT GCT CAG CGG TGG CA

The oligonucleotide 2269-69 overlaps the glycine linker and Fc portion of the template by 24 nucleotides, with the PCR resulting in the two genes being fused together in the correct reading frame.

The PCR gene product (the full length fusion gene) was digested with restriction endonucleases NdeI and BamHI, and then ligated into the vector pAMG21 and transformed into competent E. coli strain 2596 cells as described for EMP-Fc herein. Clones were screened for the ability to produce the recombinant protein product and to possess the gene fusion having the correct nucleotide sequence. A single such clone was selected and designated Amgen strain #4505.

The nucleotide and amino acid sequences (SEQ ID NOS: 1061 and 1062) of the fusion protein are shown in Figures 22A and 22B. Expression and purification were carried out as in previous examples.

Characterization of Fc-IL-1 antagonist peptide and IL-1 antagonist peptide-Fc activity. IL-1 Receptor Binding competition between IL-1β, IL-1RA and Fc-conjugated IL-1 peptide sequences was carried out using the IGEN system. Reactions contained 0.4 nM biotin-IL-1R + 15 nM IL-1-TAG + 3 uM competitor + 20 ug/ml streptavidin-conjugate beads, where competitors were IL-1RA, Fc-IL-1 antagonist, IL-1 antagonist-Fc). Competition was assayed over a range of competitor concentrations from 3 uM to 1.5 pM. The results are shown in Table C below:

Table C—Results from IL-1 Receptor Binding Competition Assay

	IL-1pep-Fc	*Fc-IL-1pep*	*IL-1ra*
KI	281.5	59.58	1.405
EC50	530.0	112.2	2.645
95% Confidence Intervals			
EC50	280.2 to 1002	54.75 to 229.8	1.149 to 6.086
KI	148.9 to 532.5	29.08 to 122.1	0.6106 to 3.233
Goodness of Fit			
R^2	0.9790	0.9687	0.9602

Example 6

VEGF-Antagonists

Fc-VEGF Antagonist. A DNA sequence coding for the Fc region of human IgG1 fused in-frame to a monomer of the VEGF mimetic peptide was constructed using standard PCR technology. The templates for the PCR reaction were the pFc-A3 plasmid and a synthetic VEGF mimetic peptide gene. The synthetic gene was assembled by annealing the following two oligonucleotides primer (SEQ ID NOS: 1120 and 1121, respectively):

```
2293-11     GTT GAA CCG AAC TGT GAC ATC CAT GTT ATG TGG GAA TGG GAA
            TGT TTT GAA CGT CTG

2293-12     CAG ACG TTC AAA ACA TTC CCA TTC CCA CAT AAC ATG GAT GTC
            ACA GTT CGG TTC AAC
```

The two oligonucleotides anneal to form the following duplex encoding an amino acid sequence shown below (SEQ ID NOS 1122):

```
            GTTGAACCGAACTGTGACATCCATGTTATGTGGGAATGGGAATGTTTTGAACGTCTG
          1 ---------+---------+---------+---------+---------+--------- 57
            CAACTTGGCTTGACACTGTAGGTACAATACACCCTTACCCTTACAAAACTTGCAGAC

a           V  E  P  N  C  D  I  H  V  M  W  E  W  E  C  F  E  R  L
-
```

This duplex was amplified in a PCR reaction using 2293-05 and 2293-06 as the sense and antisense primers (SEQ ID NOS. 1125 and 1126).

The Fc portion of the molecule was generated in a PCR reaction with the pFc-A3 plasmid using the primers 2293-03 and 2293-04 as the sense and antisense primers (SEQ ID NOS. 1123 and 1124, respectively). The full length fusion gene was obtained from a third PCR reaction using the outside primers 2293-03 and 2293-06. These primers are shown below:

2293-03 ATT TGA TTC TAG AAG GAG GAA TAA CAT ATG GAC AAA ACT CAC ACA TGT

2293-04 GTC ACA GTT CGG TTC AAC ACC ACC ACC ACC ACC TTT ACC CGG AGA CAG GGA

2293-05 TCC CTG TCT CCG GGT AAA GGT GGT GGT GGT GGT GTT GAA CCG AAC TGT GAC ATC

2293-06 CCG CGG ATC CTC GAG TTA CAG ACG TTC AAA ACA TTC CCA

The PCR gene product (the full length fusion gene) was digested with restriction endonucleases NdeI and BamHI, and then ligated into the vector pAMG21 and transformed into competent E. coli strain 2596 cells as described for EMP-Fc herein. Clones were screened for the ability to produce the recombinant protein product and to possess the gene fusion having the correct nucleotide sequence. A single such clone was selected and designated Amgen strain #4523.

The nucleotide and amino acid sequences (SEQ ID NOS: 1063 and 1064) of the fusion protein are shown in Figures 23A and 23B.

VEGF antagonist -Fc. A DNA sequence coding for a VEGF mimetic peptide fused in-frame to the Fc region of human IgG1 was constructed using standard PCR technology. The templates for the PCR reaction were the pFc-A3 plasmid and the synthetic VEGF mimetic peptide gene described above. The synthetic duplex was amplified in a PCR reaction using 2293-07 and 2293-08 as the sense and antisense primers (SEQ ID NOS. 1127 and 1128, respectively).

The Fc portion of the molecule was generated in a PCR reaction with the pFc-A3 plasmid using the primers 2293-09 and 2293-10 as the sense and antisense primers (SEQ ID NOS. 1129 and 1130, respectively).

The full length fusion gene was obtained from a third PCR reaction using the outside primers 2293-07 and 2293-10. These primers are shown below:

2293-07 ATT TGA TTC TAG AAG GAG GAA TAA CAT ATG GTT GAA CCG AAC TGT GAC

2293-08 ACA TGT GTG AGT TTT GTC ACC ACC ACC ACC ACC CAG ACG TTC AAA ACA TTC

2293-09 GAA TGT TTT GAA CGT CTG GGT GGT GGT GGT GGT GAC AAA ACT CAC ACA TGT

2293-10 CCG CGG ATC CTC GAG TTA TTT ACC CGG AGA CAG GGA GAG

The PCR gene product (the full length fusion gene) was digested with restriction endonucleases NdeI and BamHI, and then ligated into the vector pAMG21 and transformed into competent E. coli strain 2596 cells as described for EMP-Fc herein. Clones were screened for the ability to produce the recombinant protein product and to possess the gene fusion having the correct nucleotide sequence. A single such clone was selected and designated Amgen strain #4524.

The nucleotide and amino acid sequences (SEQ ID NOS: 1065 and 1066) of the fusion protein are shown in Figures 24A and 24B. Expression and purification were carried out as in previous examples.

Example 7

MMP Inhibitors

Fc-MMP inhibitor. A DNA sequence coding for the Fc region of human IgG1 fused in-frame to a monomer of an MMP inhibitory peptide was constructed using standard PCR technology. The Fc and 5 glycine linker portion of the molecule was generated in a PCR reaction with DNA from the Fc-TNF-α inhibitor fusion strain #4544 (see Example 4) using the sense primer 1216-52 and the antisense primer 2308-67 (SEQ ID NOS: 1112

and 1131, respectively). The nucleotides encoding the MMP inhibitor peptide were provided by the PCR primer 2308-67 shown below:

```
1216-52      AAC ATA AGT ACC TGT AGG ATC G

2308-67      CCG CGG ATC CAT TAG CAC AGG GTG AAA CCC CAG TGG GTG GTG
             CAA CCA CCA CCT CCA CCT TTA CCC
```

The oligonucleotide 2308-67 overlaps the glycine linker and Fc portion of the template by 22 nucleotides, with the PCR resulting in the two genes being fused together in the correct reading frame.

The PCR gene product (the full length fusion gene) was digested with restriction endonucleases NdeI and BamHI, and then ligated into the vector pAMG21 and transformed into competent E. coli strain 2596 cells as described for EMP-Fc herein. Clones were screened for the ability to produce the recombinant protein product and to possess the gene fusion having the correct nucleotide sequence. A single such clone was selected and designated Amgen strain #4597.

The nucleotide and amino acid sequences (SEQ ID NOS: 1067 and 1068) of the fusion protein are shown in Figures 25A and 25B. Expression and purification were carried out as in previous examples.

MMP Inhibitor-Fc. A DNA sequence coding for an MMP inhibitory peptide fused in-frame to the Fc region of human IgG1 was constructed using standard PCR technology. The Fc and 5 glycine linker portion of the molecule was generated in a PCR reaction with DNA from the Fc-TNF-α inhibitor fusion strain #4543 (see Example 4). The nucleotides encoding the MMP inhibitory peptide were provided by the sense PCR primer 2308-66, with primer 1200-54 serving as the antisense primer (SEQ ID NOS: 1132 and 407, respectively). The primer sequences are shown below:

```
2308-66      GAA TAA CAT ATG TGC ACC ACC CAC TGG GGT TTC ACC CTG TGC
             GGT GGA GGC GGT GGG GAC AAA

1200-54      GTT ATT GCT CAG CGG TGG CA
```

The oligonucleotide 2269-69 overlaps the glycine linker and Fc portion of the template by 24 nucleotides, with the PCR resulting in the two genes being fused together in the correct reading frame.

The PCR gene product (the full length fusion gene) was digested with restriction endonucleases NdeI and BamHI, and then ligated into the vector pAMG21 and transformed into competent E. coli strain 2596 cells as described for EMP-Fc herein. Clones were screened for the ability to produce the recombinant protein product and to possess the gene fusion having the correct nucleotide sequence. A single such clone was selected and designated Amgen strain #4598.

The nucleotide and amino acid sequences (SEQ ID NOS: 1069 and 1070) of the fusion protein are shown in Figures 26A and 26B.

* * *

The invention now being fully described, it will be apparent to one of ordinary skill in the art that many changes and modifications can be made thereto, without departing from the spirit and scope of the invention as set forth herein.

Abbreviations

Abbreviations used throughout this specification are as defined below, unless otherwise defined in specific circumstances.

Ac	acetyl (used to refer to acetylated residues)
AcBpa	acetylated p-benzoyl-L-phenylalanine
ADCC	antibody-dependent cellular cytotoxicity
Aib	aminoisobutyric acid
bA	beta-alanine
Bpa	p-benzoyl-L-phenylalanine
BrAc	bromoacetyl ($BrCH_2C(O)$)

BSA	Bovine serum albumin
Bzl	Benzyl
Cap	Caproic acid
CTL	Cytotoxic T lymphocytes
CTLA4	Cytotoxic T lymphocyte antigen 4
DARC	Duffy blood group antigen receptor
DCC	Dicylcohexylcarbodiimide
Dde	1-(4,4-dimethyl-2,6-dioxo-cyclohexylidene)ethyl
EMP	Erythropoietin-mimetic peptide
ESI-MS	Electron spray ionization mass spectrometry
EPO	Erythropoietin
Fmoc	fluorenylmethoxycarbonyl
G-CSF	Granulocyte colony stimulating factor
GH	Growth hormone
HCT	hematocrit
HGB	hemoglobin
hGH	Human growth hormone
HOBt	1-Hydroxybenzotriazole
HPLC	high performance liquid chromatography
IL	interleukin
IL-R	interleukin receptor
IL-1R	interleukin-1 receptor
IL-1ra	interleukin-1 receptor antagonist
Lau	Lauric acid
LPS	lipopolysaccharide
LYMPH	lymphocytes
MALDI-MS	Matrix-assisted laser desorption ionization mass spectrometry
Me	methyl

MeO	methoxy
MHC	major histocompatibility complex
MMP	matrix metalloproteinase
MMPI	matrix metalloproteinase inhibitor
1-Nap	1-napthylalanine
NEUT	neutrophils
NGF	nerve growth factor
Nle	norleucine
NMP	N-methyl-2-pyrrolidinone
PAGE	polyacrylamide gel electrophoresis
PBS	Phosphate-buffered saline
Pbf	2,2,4,6,7-pendamethyldihydrobenzofuran-5-sulfonyl
PCR	polymerase chain reaction
Pec	pipecolic acid
PEG	Poly(ethylene glycol)
pGlu	pyroglutamic acid
Pic	picolinic acid
PLT	platelets
pY	phosphotyrosine
RBC	red blood cells
RBS	ribosome binding site
RT	room temperature (25 °C)
Sar	sarcosine
SDS	sodium dodecyl sulfate
STK	serine-threonine kinases
t-Boc	tert-Butoxycarbonyl
tBu	tert-Butyl
TGF	tissue growth factor
THF	thymic humoral factor

TK	tyrosine kinase
TMP	Thrombopoietin-mimetic peptide
TNF	Tissue necrosis factor
TPO	Thrombopoietin
TRAIL	TNF-related apoptosis-inducing ligand
Trt	trityl
UK	urokinase
UKR	urokinase receptor
VEGF	vascular endothelial cell growth factor
VIP	vasoactive intestinal peptide
WBC	white blood cells

What is claimed is:

1. A composition of matter of the formula

$$(X^1)_a\text{-}F^1\text{-}(X^2)_b$$

and multimers thereof, wherein:

F^1 is an Fc domain;

X^1 and X^2 are each independently selected from $-(L^1)_c\text{-}P^1$, $-(L^1)_c\text{-}P^1\text{-}(L^2)_d\text{-}P^2$, $-(L^1)_c\text{-}P^1\text{-}(L^2)_d\text{-}P^2\text{-}(L^3)_e\text{-}P^3$, and $-(L^1)_c\text{-}P^1\text{-}(L^2)_d\text{-}P^2\text{-}(L^3)_e\text{-}P^3\text{-}(L^4)_f\text{-}P^4$

P^1, P^2, P^3, and P^4 are each independently sequences of pharmacologically active peptides;

L^1, L^2, L^3, and L^4 are each independently linkers; and

a, b, c, d, e, and f are each independently 0 or 1, provided that at least one of a and b is 1.

2. The composition of matter of Claim 1 of the formulae

$$X^1\text{-}F^1$$

or

$$F^1\text{-}X^2.$$

3. The composition of matter of Claim 1 of the formula

$$F^1\text{-}(L^1)_c\text{-}P^1.$$

4. The composition of matter of Claim 1 of the formula

$$F^1\text{-}(L^1)_c\text{-}P^1\text{-}(L^2)_d\text{-}P^2.$$

5. The composition of matter of Claim 1 wherein F^1 is an IgG Fc domain.

6. The composition of matter of Claim 1 wherein F^1 is an IgG1 Fc domain.

7. The composition of matter of Claim 1 wherein F^1 comprises the sequence of SEQ ID NO: 2.

8. The composition of matter of Claim 1 wherein X^1 and X^2 comprise an IL-1 antagonist peptide sequence.

9. The composition of matter of Claim 8 wherein the IL-1 antagonist peptide sequence is selected from SEQ ID NOS: 212, 907, 908, 909, 910, 917, and 979.

10. The composition of matter of Claim 8 wherein the IL-1 antagonist peptide sequence is selected from SEQ ID NOS: 213 to 271, 671 to 906, 911 to 916, and 918 to 1023.

11. The composition of matter of Claim 8 wherein F^1 comprises the sequence of SEQ ID NO: 2.

12. The composition of matter of Claim 1 wherein X^1 and X^2 comprise an EPO-mimetic peptide sequence.

13. The composition of matter of Claim 12 wherein the EPO-mimetic peptide sequence is selected from Table 5.

14. The composition of matter of Claim 12 wherein F^1 comprises the sequence of SEQ ID NO: 2.

15. The composition of matter of Claim 12 comprising a sequence selected from SEQ ID NOS: 83, 84, 85, 124, 419, 420, 421, and 461. .

16. The composition of matter of claim 12 comprising a sequence selected from SEQ ID NOS: 339 and 340.

17. The composition of matter of Claim 12 comprising a sequence selected from SEQ ID NOS: 20 and 22.

18. The composition of matter of Claim 3 wherein P^1 is a TPO-mimetic peptide sequence.

19. The composition of matter of Claim 18 wherein P^1 is a TPO-mimetic peptide sequence selected from Table 6.

20. The composition of matter of Claim 18 wherein F^1 comprises the sequence of SEQ ID NO: 2.

21. The composition of matter of Claim 18 having a sequence selected from SEQ ID NOS: 6 and 12.

22. A DNA encoding a composition of matter of any of Claims 1 to 21.

23. An expression vector comprising the DNA of Claim 22.

24. A host cell comprising the expression vector of Claim 23.

25. The cell of Claim 24, wherein the cell is an E. coli cell.

26. A process for preparing a pharmacologically active compound, which comprises

a) selecting at least one randomized peptide that modulates the activity of a protein of interest; and

b) preparing a pharmacologic agent comprising at least one Fc domain covalently linked to at least one amino acid sequence of the selected peptide or peptides.

27. The process of Claim 26, wherein the peptide is selected in a process comprising screening of a phage display library, an E. coli display library, a ribosomal library, or a chemical peptide library.

28. The process of Claim 26, wherein the preparation of the pharmacologic agent is carried out by:

a) preparing a gene construct comprising a nucleic acid sequence encoding the selected peptide and a nucleic acid sequence encoding an Fc domain; and

b) expressing the gene construct.

29. The process of Claim 26, wherein the gene construct is expressed in an E. coli cell.

30. The process of Claim 26, wherein the protein of interest is a cell surface receptor.

31. The process of Claim 26, wherein the protein of interest has a linear epitope.

32. The process of Claim 26, wherein the protein of interest is a cytokine receptor.

33. The process of Claim 26, wherein the peptide is an EPO-mimetic peptide.

34. The process of Claim 26, wherein the peptide is a TPO-mimetic peptide.

35. The process of Claim 26, wherein the peptide is an IL-1 antagonist peptide.

36. The process of Claim 26, wherein the peptide is an MMP inhibitor peptide or a VEGF antagonist peptide.

37. The process of Claim 26, wherein the peptide is a TNF-antagonist peptide.

38. The process of Claim 26, wherein the peptide is a CTLA4-mimetic peptide.

39. The process of Claim 26, wherein the peptide is selected from Tables 4 to 20.

40. The process of Claim 26, wherein the selection of the peptide is carried out by a process comprising:

a) preparing a gene construct comprising a nucleic acid sequence encoding a first selected peptide and a nucleic acid sequence encoding an Fc domain;

b) conducting a polymerase chain reaction using the gene construct and mutagenic primers, wherein

i) a first mutagenic primer comprises a nucleic acid sequence complementary to a sequence at or near the 5′ end of a coding strand of the gene construct, and

ii) a second mutagenic primer comprises a nucleic acid sequence complementary to the 3′ end of the noncoding strand of the gene construct.

41. The process of Claim 26, wherein the compound is derivatized.

42. The process of Claim 26, wherein the derivatized compound comprises a cyclic portion, a cross-linking site, a non-peptidyl

linkage, an N-terminal replacement, a C-terminal replacement, or a modified amino acid moiety.

43. The process of Claim 26 wherein the Fc domain is an IgG Fc domain.

44. The process of Claim 26, wherein the vehicle is an IgG1 Fc domain.

45. The process of Claim 26, wherein the vehicle comprises the sequence of SEQ ID NO: 2.

46. The process of Claim 26, wherein the compound prepared is of the formula

$$(X^1)_a\text{-}F^1\text{-}(X^2)_b$$

and multimers thereof,wherein:

F^1 is an Fc domain;

X^1 and X^2 are each independently selected from $-(L^1)_c\text{-}P^1$, $-(L^1)_c\text{-}P^1\text{-}(L^2)_d\text{-}P^2$, $-(L^1)_c\text{-}P^1\text{-}(L^2)_d\text{-}P^2\text{-}(L^3)_e\text{-}P^3$, and $-(L^1)_c\text{-}P^1\text{-}(L^2)_d\text{-}P^2\text{-}(L^3)_e\text{-}P^3\text{-}(L^4)_f\text{-}P^4$

P^1, P^2, P^3, and P^4 are each independently sequences of pharmacologically active peptides;

L^1, L^2, L^3, and L^4 are each independently linkers; and

a, b, c, d, e, and f are each independently 0 or 1, provided that at least one of a and b is 1.

47. The process of Claim 46, wherein the compound prepared is of the formulae

$$X^1\text{-}F^1$$

or

$$F^1\text{-}X^2.$$

48. The process of Claim 46, wherein the compound prepared is of the formulae

$$F^1\text{-}(L^1)_c\text{-}P^1$$

or

$$F^1\text{-}(L^1)_c\text{-}P^1\text{-}(L^2)_d\text{-}P^2.$$

49. The process of Claim 46, wherein F^1 is an IgG Fc domain.

50. The process of Claim 46, wherein F^1 is an IgG1 Fc domain.

51. The process of Claim 46, wherein F^1 comprises the sequence of SEQ ID NO: 2.